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        Ling, Ai Ee
        Ooi, Eng Eong
        Chng, Hiok Hee

<120>   Diagnostics for SARS Virus

<130>   2577-162

<150>   60/486,918
<151>   2003-07-15

<150>   PCT/US04/003307
<151>   2004-02-04

<160>   25

<170>   PatentIn version 3.2

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aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat gga gga      96
Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
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cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat     144
Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
        35                  40                  45

aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa     192
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
    50                  55                  60

ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat agt ggt     240
Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65                  70                  75                  80

cca gat gac caa att ggc tac tac cga aga gct acc cga cga gtt cgt     288
Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
                85                  90                  95
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ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac ttc tat    336
Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
            100                 105                 110

tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct aac aaa    384
Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
            115                 120                 125

gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca ccc aaa    432
Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
        130                 135                 140

gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc gtg cta    480
Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145                 150                 155                 160

caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca gag gga    528
Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
                165                 170                 175

agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt agt cgc    576
Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
            180                 185                 190

ggt aat tca aga aat tca act cct ggc agc agt agg gga aat tct cct    624
Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
            195                 200                 205

gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta ttg ctg    672
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cta gac aga ttg aac cag ctt gag agc aaa gtt tct ggt aaa ggc caa    720
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225                 230                 235                 240

caa caa caa ggc caa act gtc act aag aaa tct gct gct gag gca tct    768
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aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac gtc act    816
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            260                 265                 270

caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat ttc ggg    864
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            275                 280                 285

gac caa gac cta atc aga caa gga act gat tac aaa cat tgg ccg caa    912
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att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg tca cgc    960
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2

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gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata       1056
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ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca aca gag       1104
Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
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cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg       1152
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cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg gct gac       1200
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385                     390                     395                     400

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Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
              130   135   140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145   150   155   160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
              165   170   175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
              180   185   190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
              195   200   205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
              210   215   220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225   230   235   240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
              245   250   255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
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Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
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Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
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        340             345             350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
        355             360             365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
    370             375             380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
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Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
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Ala Asp Ser Thr Gln Ala
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1               5                   10                  15

gac cgg tgc acc act ttt gat gat gtt caa gct cct aat tac act caa      96
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20                  25                  30
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cat act tca tct atg agg ggg gtt tac tat cct gat gaa att ttt aga        144
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35                  40                  45

tca gac act ctt tat tta act cag gat tta ttt ctt cca ttt tat tct        192
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
        50                  55                  60

aat gtt aca ggg ttt cat act att aat cat acg ttt ggc aac cct gtc        240
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65                  70                  75                  80

ata cct ttt aag gat ggt att tat ttt gct gcc aca gag aaa tca aat        288
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
                85                  90                  95

gtt gtc cgt ggt tgg gtt ttt ggt tct acc atg aac aac aag tca cag        336
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100                 105                 110

tcg gtg att att att aac aat tct act aat gtt gtt ata cga gca tgt        384
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
            115                 120                 125

aac ttt gaa ttg tgt gac aac cct ttc ttt gct gtt tct aaa ccc atg        432
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
        130                 135                 140

ggt aca cag aca cat act atg ata ttc gat aat gca ttt aat tgc act        480
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145                 150                 155                 160

ttc gag tac ata tct gat gcc ttt tcg ctt gat gtt tca gaa aag tca        528
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
                165                 170                 175

ggt aat ttt aaa cac tta cga gag ttt gtg ttt aaa aat aaa gat ggg        576
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
                180                 185                 190

ttt ctc tat gtt tat aag ggc tat caa cct ata gat gta gtt cgt gat        624
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
            195                 200                 205

cta cct tct ggt ttt aac act ttg aaa cct att ttt aag ttg cct ctt        672
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
        210                 215                 220

ggt att aac att aca aat ttt aga gcc att ctt aca gcc ttt tca cct        720
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225                 230                 235                 240

gct caa gac att tgg ggc acg tca gct gca gcc tat ttt gtt ggc tat        768
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
                245                 250                 255
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6

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tta aag cca act aca ttt atg ctc aag tat gat gaa aat ggt aca atc       816
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
            260             265                 270

aca gat gct gtt gat tgt tct caa aat cca ctt gct gaa ctc aaa tgc       864
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
            275             280                 285

tct gtt aag agc ttt gag att gac aaa gga att tac cag acc tct aat       912
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
            290             295                 300

ttc agg gtt gtt ccc tca gga gat gtt gtg aga ttc cct aat att aca       960
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305             310                 315                 320

aac ttg tgt cct ttt gga gag gtt ttt aat gct act aaa ttc cct tct      1008
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
                325             330                 335

gtc tat gca tgg gag aga aaa aaa att tct aat tgt gtt gct gat tac      1056
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
                340             345                 350

tct gtg ctc tac aac tca aca ttt ttt tca acc ttt aag tgc tat ggc      1104
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
            355             360                 365

gtt tct gcc act aag ttg aat gat ctt tgc ttc tcc aat gtc tat gca      1152
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370             375                 380

gat tct ttt gta gtc aag gga gat gat gta aga caa ata gcg cca gga      1200
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385             390                 395                 400

caa act ggt gtt att gct gat tat aat tat aaa ttg cca gat gat ttc      1248
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
                405             410                 415

atg ggt tgt gtc ctt gct tgg aat act agg aac att gat gct act tca      1296
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
                420             425                 430

act ggt aat tat aat tat aaa tat agg tat ctt aga cat ggc aag ctt      1344
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
            435             440                 445

agg ccc ttt gag aga gac ata tct aat gtg cct ttc tcc cct gat ggc      1392
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450             455                 460

aaa cct tgc acc cca cct gct ctt aat tgt tat tgg cca tta aat gat      1440
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
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7

tat ggt ttt tac acc act act ggc att ggc tac caa cct tac aga gtt   1488
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gta gta ctt tct ttt gaa ctt tta aat gca ccg gcc acg gtt tgt gga   1536
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
                500   505   510

cca aaa tta tcc act gac ctt att aag aac cag tgt gtc aat ttt aat   1584
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
                515   520   525

ttt aat gga ctc act ggt act ggt gtg tta act cct tct tca aag aga   1632
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
                530   535   540

ttt caa cca ttt caa caa ttt ggc cgt gat gtt tct gat ttc act gat   1680
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545   550   555   560

tcc gtt cga gat cct aaa aca tct gaa ata tta gac att tca cct tgc   1728
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565   570   575

tct ttt ggg ggt gta agt gta att aca cct gga aca aat gct tca tct   1776
Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
                580   585   590

gaa gtt gct gtt cta tat caa gat gtt aac tgc act gat gtt tct aca   1824
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
                595   600   605

gca att cat gca gat caa ctc aca cca gct tgg cgc ata tat tct act   1872
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
                610   615   620

gga aac aat gta ttc cag act caa gca ggc tgt ctt ata gga gct gag   1920
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625   630   635   640

cat gtc gac act tct tat gag tgc gac att cct att gga gct ggc att   1968
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
                645   650   655

tgt gct agt tac cat aca gtt tct tta tta cgt agt act agc caa aaa   2016
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
                660   665   670

tct att gtg gct tat act atg tct tta ggt gct gat agt tca att gct   2064
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
                675   680   685

tac tct aat aac acc att gct ata cct act aac ttt tca att agc att   2112

8

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Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690                     695                 700

act aca gaa gta atg cct gtt tct atg gct aaa acc tcc gta gat tgt        2160
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705                     710                 715                 720

aat atg tac atc tgc gga gat tct act gaa tgt gct aat ttg ctt ctc        2208
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725                 730                 735

caa tat ggt agc ttt tgc aca caa cta aat cgt gca ctc tca ggt att        2256
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740                 745                 750

gct gct gaa cag gat cgc aac aca cgt gaa gtg ttc gct caa gtt aaa        2304
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
            755                 760                 765

caa atg tac aaa acc cca act ttg aaa tat ttt ggt ggt ttt aat ttt        2352
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
        770                 775                 780

tca caa ata tta cct gac cct cta aag cca act aag agg tct ttt att        2400
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785                 790                 795                 800

gag gac ttg ctc ttt aat aag gtg aca ctc gct gat gct ggc ttc atg        2448
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
                805                 810                 815

aag caa tat ggc gaa tgc cta ggt gat att aat gct aga gat ctc att        2496
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820                 825                 830

tgt gcg cag aag ttc aat gga ctt aca gtg ttg cca cct ctg ctc act        2544
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
            835                 840                 845

gat gat atg att gct gcc tac act gct gct cta gtt agt ggt act gcc        2592
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
            850                 855                 860

act gct gga tgg aca ttt ggt gct ggc gct gct ctt caa ata cct ttt        2640
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865                 870                 875                 880

gct atg caa atg gca tat agg ttc aat ggc att gga gtt acc caa aat        2688
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
                885                 890                 895

gtt ctc tat gag aac caa aaa caa atc gcc aac caa ttt aac aag gcg        2736
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            900                 905                 910
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9

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att agt caa att caa gaa tca ctt aca aca aca tca act gca ttg ggc        2784
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        915                 920                 925


aag ctg caa gac gtt gtt aac cag aat gct caa gca tta aac aca ctt        2832
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
        930                 935                 940


gtt aaa caa ctt agc tct aat ttt ggt gca att tca agt gtg cta aat        2880
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945                 950            .    955                 960


gat atc ctt tcg cga ctt gat aaa gtc gag gcg gag gta caa att gac        2928
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                965                 970                 975


agg tta att aca ggc aga ctt caa agc ctt caa acc tat gta aca caa        2976
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
                980                 985                 990


caa cta atc agg gct gct gaa atc  agg gct tct gct aat  ctt gct gct     3024
Gln Leu Ile Arg Ala Ala Glu Ile  Arg Ala Ser Ala Asn  Leu Ala Ala
        995                 1000                 1005


act aaa  atg tct gag tgt gtt  ctt gga caa tca aaa  aga gtt gac        3069
Thr Lys  Met Ser Glu Cys Val  Leu Gly Gln Ser Lys  Arg Val Asp
        1010                 1015                 1020


ttt tgt  gga aag ggc tac cac  ctt atg tcc ttc cca  caa gca gcc        3114
Phe Cys  Gly Lys Gly Tyr His  Leu Met Ser Phe Pro  Gln Ala Ala
        1025                 1030                 1035


ccg cat  ggt gtt gtc ttc cta  cat gtc acg tat gtg  cca tcc cag        3159
Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro Ser Gln
        1040                 1045                 1050


gag agg  aac ttc acc aca gcg  cca gca att tgt cat  gaa ggc aaa        3204
Glu Arg  Asn Phe Thr Thr Ala  Pro Ala Ile Cys His  Glu Gly Lys
        1055                 1060                 1065


gca tac  ttc cct cgt gaa ggt  gtt ttt gtg ttt aat  ggc act tct        3249
Ala Tyr  Phe Pro Arg Glu Gly  Val Phe Val Phe Asn  Gly Thr Ser
        1070                 1075                 1080


tgg ttt  att aca cag agg aac  ttc ttt tct cca caa  ata att act        3294
Trp Phe  Ile Thr Gln Arg Asn  Phe Phe Ser Pro Gln  Ile Ile Thr
        1085                 1090                 1095


aca gac  aat aca ttt gtc tca  gga aat tgt gat gtc  gtt att ggc        3339
Thr Asp  Asn Thr Phe Val Ser  Gly Asn Cys Asp Val  Val Ile Gly
        1100                 1105                 1110


atc att  aac aac aca gtt tat  gat cct ctg caa cct  gag ctt gac        3384
Ile Ile  Asn Asn Thr Val Tyr  Asp Pro Leu Gln Pro  Glu Leu Asp
        1115                 1120                 1125
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10

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tca ttc aaa gaa gag ctg gac  aag tac ttc aaa aat  cat aca tca      3429
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cca gat gtt gat ctt ggc gac  att tca ggc att aac  gct tct gtc      3474
Pro Asp Val Asp Leu Gly Asp  Ile Ser Gly Ile Asn  Ala Ser Val
    1145              1150             1155

gtc aac att caa aaa gaa att  gac cgc ctc aat gag  gtc gct aaa      3519
Val Asn Ile Gln Lys Glu Ile  Asp Arg Leu Asn Glu  Val Ala Lys
    1160              1165             1170

aat tta aat gaa tca ctc att  gac ctt caa gaa ttg  gga aaa tat      3564
Asn Leu Asn Glu Ser Leu Ile  Asp Leu Gln Glu Leu  Gly Lys Tyr
    1175              1180             1185

gag caa tat att aaa tgg cct  tgg tat gtt tgg ctc  ggc ttc att      3609
Glu Gln Tyr Ile Lys Trp Pro  Trp Tyr Val Trp Leu  Gly Phe Ile
    1190              1195             1200

gct gga cta att gcc atc gtc  atg gtt aca atc ttg  ctt tgt tgc      3654
Ala Gly Leu Ile Ala Ile Val  Met Val Thr Ile Leu  Leu Cys Cys
    1205              1210             1215

atg act agt tgt tgc agt tgc  ctc aag ggt gca tgc  tct tgt ggt      3699
Met Thr Ser Cys Cys Ser Cys  Leu Lys Gly Ala Cys  Ser Cys Gly
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tct tgc tgc aag ttt gat gag  gat gac tct gag cca  gtt ctc aag      3744
Ser Cys Cys Lys Phe Asp Glu  Asp Asp Ser Glu Pro  Val Leu Lys
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<210>   4
<211>   1255
<212>   PRT
<213>   SARS coronavirus

<400>   4

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1               5              10             15


Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
            20             25             30


His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
        35             40             45
```

11

```
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50              55                  60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65              70                  75                  80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
            85                  90                  95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
            100             105             110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
            115             120             125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
    130             135             140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145             150             155             160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
            165             170             175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180             185             190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
            195             200             205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
    210             215             220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225             230             235             240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
            245             250             255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
```

12

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
    275   280   285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
    290   295   300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305   310   315   320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
          325   330   335

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
        340   345   350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
        355   360   365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
    370   375   380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385   390   395   400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
        405   410   415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
        420   425   430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
        435   440   445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
    450   455   460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465   470   475   480

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
                    485   490   495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
            500   505   510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
            515   520   525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
        530   .   535   540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545   550   555   560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565   570   575

Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
            580   585   590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
            595   600   605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
        610   615   620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625   630   635   640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
                645   650   655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
                660   665   670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
            675   680   685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690   695   700

14

```
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705             710             715             720


Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
                725             730             735


Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740             745             750


Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
            755             760             765


Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
    770             775             780


Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785             790             795             800


Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
            805             810             815


Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820             825             830


Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
            835             840             845


Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
    850             855             860


Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865             870             875             880


Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
            885             890             895


Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900             905             910


Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
    915             920             925
```

15

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
    930   935   940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945   950   955   960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
                  965   970   975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
                  980   985   990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
                  995   1000   1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
    1010   1015   1020

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
    1025   1030   1035

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
    1040   1045   1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
    1055   1060   1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
    1070   1075   1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
    1085   1090   1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
    1100   1105   1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
    1115   1120   1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser

16

```
                 1130                          1135                          1140


Pro Asp  Val Asp Leu Gly Asp  Ile Ser Gly Ile Asn  Ala Ser Val
    1145                      1150                  1155


Val Asn  Ile Gln Lys Glu Ile  Asp Arg Leu Asn Glu  Val Ala Lys
    1160                      1165.                 1170


Asn Leu  Asn Glu Ser Leu Ile  Asp Leu Gln Glu Leu  Gly Lys Tyr
    1175                      1180                  1185


Glu Gln  Tyr Ile Lys Trp Pro  Trp Tyr Val Trp Leu  Gly Phe Ile
    1190                      1195                  1200


Ala Gly  Leu Ile Ala Ile Val  Met Val Thr Ile Leu  Leu Cys Cys
    1205                      1210                  1215


Met Thr  Ser Cys Cys Ser Cys  Leu Lys Gly Ala Cys  Ser Cys Gly
    1220                      1225                  1230


Ser Cys  Cys Lys Phe Asp Glu  Asp Asp Ser Glu Pro  Val Leu Lys
    1235                      1240                  1245


Gly Val  Lys Leu His Tyr Thr
    1250                      1255



<210>  5
<211>  588
<212>  DNA
<213>  SARS coronavirus


<220>
<221>  CDS
<222>  (1)..(588)

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ttg aac cag ctt gag agc aaa gtt tct ggt aaa ggc caa caa caa caa     48
Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln Gln Gln Gln
1                   5                   10                  15


ggc caa act gtc act aag aaa tct gct gct gag gca tct aaa aag cct     96
Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro
            20                  25                  30


cgc caa aaa cgt act gcc aca aaa cag tac aac gtc act caa gca ttt    144
```

```
Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr Gln Ala Phe
        35              40              45

ggg aga cgt ggt cca gaa caa acc caa gga aat ttc ggg gac caa gac    192
Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly Asp Gln Asp
        50              55              60

cta atc aga caa gga act gat tac aaa cat tgg ccg caa att gca caa    240
Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln Ile Ala Gln
65              70              75              80

ttt gct cca agt gcc tct gca ttc ttt gga atg tca cgc att ggc atg    288
Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg Ile Gly Met
            85              90              95

gaa gtc aca cct tcg gga aca tgg ctg act tat cat gga gcc att aaa    336
Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly Ala Ile Lys
            100             105             110

ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata ctg ctg aac    384
Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile Leu Leu Asn
            115             120             125

aag cac att gac gca tac aaa aca ttc cca cca aca gag cct aaa aag    432
Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys
        130             135             140

gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg cag aga caa    480
Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro Gln Arg Gln
145             150             155             160

aag aag cag ccc act gtg act ctt ctt cct gcg gct gac atg gat gat    528
Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp Met Asp Asp
            165             170             175

ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct gct gat tca    576
Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser Ala Asp Ser
            180             185             190

act cag gca taa                                                    588
Thr Gln Ala
        195


<210>   6
<211>   195
<212>   PRT
<213>   SARS coronavirus

<400>   6

Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln Gln Gln Gln
1               5               10              15
```

18

```
Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro
            20                  25                  30

Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr Gln Ala Phe
            35                  40                  45

Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly Asp Gln Asp
            50                  55                  60

Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln Ile Ala Gln
65                  70                  75                  80

Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg Ile Gly Met
            85                  90                  95

Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly Ala Ile Lys
            100                 105                 110

Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile Leu Leu Asn
            115                 120                 125

Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys
    130                 135                 140

Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro Gln Arg Gln
145                 150                 155                 160

Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp Met Asp Asp
            165                 170                 175

Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser Ala Asp Ser
            180                 185                 190

Thr Gln Ala
        195


<210>   7
<211>   684
<212>   DNA
<213>   SARS coronavirus


<220>
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19

<221> CDS
<222> (1)..(684)

<400> 7

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agg tat ctt aga cat ggc aag ctt agg ccc ttt gag aga gac ata tct        48
Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser
1               5                   10                  15

aat gtg cct ttc tcc cct gat ggc aaa cct tgc acc cca cct gct ctt        96
Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu
            20                  25                  30

aat tgt tat tgg cca tta aat gat tat ggt ttt tac acc act act ggc       144
Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly
            35                  40                  45

att ggc tac caa cct tac aga gtt gta gta ctt tct ttt gaa ctt tta       192
Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
        50                  55                  60

aat gca ccg gcc acg gtt tgt gga cca aaa tta tcc act gac ctt att       240
Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile
65                  70                  75                  80

aag aac cag tgt gtc aat ttt aat ttt aat gga ctc act ggt act ggt       288
Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
                85                  90                  95

gtg tta act cct tct tca aag aga ttt caa cca ttt caa caa ttt ggc       336
Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly
            100                 105                 110

cgt gat gtt tct gat ttc act gat tcc gtt cga gat cct aaa aca tct       384
Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser
            115                 120                 125

gaa ata tta gac att tca cct tgc tct ttt ggg ggt gta agt gta att       432
Glu Ile Leu Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile
        130                 135                 140

aca cct gga aca aat gct tca tct gaa gtt gct gtt cta tat caa gat       480
Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp
145                 150                 155                 160

gtt aac tgc act gat gtt tct aca gca att cat gca gat caa ctc aca       528
Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
                165                 170                 175

cca gct tgg cgc ata tat tct act gga aac aat gta ttc cag act caa       576
Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
            180                 185                 190

gca ggc tgt ctt ata gga gct gag cat gtc gac act tct tat gag tgc       624
Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
        195                 200                 205
```

20

```
gac att cct att gga gct ggc att tgt gct agt tac cat aca gtt tct        672
Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
    210             215             220

tta tta cgt agt                                                        684
Leu Leu Arg Ser
225
```

```
Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser
1               5               10              15


Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu
            20              25              30


Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly
            35              40              45


Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
    50              55              60


Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile
65              70              75              80


Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
            85              90              95


Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly
            100             105             110


Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser
        115             120             125


Glu Ile Leu Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile
    130             135             140


Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp
145             150             155             160
```

21

```
Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
                165                 170                 175


Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
            180                 185                 190


Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
            195                 200                 205


Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
    210                 215                 220


Leu Leu Arg Ser
225


<210>   9
<211>   29711
<212>   DNA
<213>   SARS coronavirus

<400>   9
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aaatctgtgt agctgtcgct cggctgcatg cctagtgcac ctacgcagta taaacaataa     120

taaattttac tgtcgttgac aagaaacgag taactcgtcc ctcttctgca gactgcttac     180

ggtttcgtcc gtgttgcagt cgatcatcag catacctagg tttcgtccgg gtgtgaccga     240

aaggtaagat ggagagcctt gttcttggtg tcaacgagaa aacacacgtc caactcagtt     300

tgcctgtcct tcaggttaga gacgtgctag tgcgtggctt cggggactct gtggaagagg     360

ccctatcgga ggcacgtgaa cacctcaaaa atggcacttg tggtctagta gagctggaaa     420

aaggcgtact gccccagctt gaacagccct atgtgttcat taaacgttct gatgccttaa     480

gcaccaatca cggccacaag gtcgttgagc tggttgcaga aatggacggc attcagtacg     540

gtcgtagcgg tataacactg ggagtactcg tgccacatgt gggcgaaacc ccaattgcat     600

accgcaatgt tcttcttcgt aagaacggta ataagggagc cggtggtcat agctatggca     660

tcgatctaaa gtcttatgac ttaggtgacg agcttggcac tgatcccatt gaagattatg     720

aacaaaactg gaacactaag catggcagtg gtgcactccg tgaactcact cgtgagctca     780

atggaggtgc agtcactcgc tatgtcgaca acaatttctg tggcccagat gggtaccctc     840
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ttgattgcat  caaagatttt  ctcgcacgcg  cgggcaagtc  aatgtgcact  ctttccgaac       900

aacttgatta  catcgagtcg  aagagaggtg  tctactgctg  ccgtgaccat  gagcatgaaa       960

ttgcctggtt  cactgagcgc  tctgataaga  gctacgagca  ccagacaccc  ttcgaaatta      1020

agagtgccaa  gaaatttgac  actttcaaag  gggaatgccc  aaagtttgtg  tttcctctta      1080

actcaaaagt  caaagtcatt  caaccacgtg  ttgaaaagaa  aaagactgag  ggtttcatgg      1140

ggcgtatacg  ctctgtgtac  cctgttgcat  ctccacagga  gtgtaacaat  atgcacttgt      1200

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ggtacctacc  tactaatgct  gtagtgaaaa  tgccatgtcc  tgcctgtcaa  gacccagaga      1380

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gcaagggagg  taggactaga  tgttttggag  gctgtgtgtt  tgcctatgtt  ggctgctata      1500

ataagcgtgc  ctactgggtt  cctcgtgcta  gtgctgatat  tggctcaggc  catactggca      1560

ttactggtga  caatgtggag  accttgaatg  aggatctcct  tgagatactg  agtcgtgaac      1620

gtgttaacat  taacattgtt  ggcgattttc  atttgaatga  agaggttgcc  atcattttgg      1680

catctttctc  tgcttctaca  agtgccttta  ttgacactat  aaagagtctt  gattacaagt      1740

ctttcaaaac  cattgttgag  tcctgcggta  actataaagt  taccaaggga  aagcccgtaa      1800

aaggtgcttg  gaacattgga  caacagagat  cagttttaac  accactgtgt  ggttttccct      1860

cacaggctgc  tggtgttatc  agatcaattt  ttgcgcgcac  acttgatgca  gcaaaccact      1920

caattcctga  tttgcaaaga  gcagctgtca  ccatacttga  tggtatttct  gaacagtcat      1980

tacgtcttgt  cgacgccatg  gtttatactt  cagacctgct  caccaacagt  gtcattatta      2040

tggcatatgt  aactggtggt  cttgtacaac  agacttctca  gtggttgtct  aatcttttgg      2100

gcactactgt  tgaaaaactc  aggcctatct  ttgaatggat  tgaggcgaaa  cttagtgcag      2160

gagttgaatt  tctcaaggat  gcttgggaga  ttctcaaatt  tctcattaca  ggtgtttttg      2220

acatcgtcaa  gggtcaaata  caggttgctt  cagataacat  caaggattgt  gtaaaatgct      2280

tcattgatgt  tgttaacaag  gcactcgaaa  tgtgcattga  tcaagtcact  atcgctggcg      2340

caaagttgcg  atcactcaac  ttaggtgaag  tcttcatcgc  tcaaagcaag  ggactttacc      2400

gtcagtgtat  acgtggcaag  gagcagctgc  aactactcat  gcctcttaag  gcaccaaaag      2460
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23

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aagtaacctt tcttgaaggt gattcacatg acacagtact tacctctgag gaggttgttc   2520

tcaagaacgg tgaactcgaa gcactcgaga cgcccgttga tagcttcaca aatggagcta   2580

tcgttggcac accagtctgt gtaaatggcc tcatgctctt agagattaag gacaaagaac   2640

aatactgcgc attgtctcct ggtttactgg ctacaaacaa tgtctttcgc ttaaaagggg   2700

gtgcaccaat taaaggtgta acctttggag aagatactgt ttgggaagtt caaggttaca   2760

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gctctgtcta cactgttgaa tccggtaccg aagttactga gtttgcatgt gttgtagcag   2880

aggctgttgt gaagacttta caaccagttt ctgatctcct taccaacatg ggtattgatc   2940

ttgatgagtg gagtgtagct acattctact tatttgatga tgctggtgaa gaaaactttt   3000

catcacgtat gtattgttcc ttttaccctc cagatgagga agaagaggac gatgcagagt   3060

gtgaggaaga agaaattgat gaaacctgtg aacatgagta cggtacagag gatgattatc   3120

aaggtctccc tctggaattt ggtgcctcag ctgaaacagt tcgagttgag gaagaagaag   3180

aggaagactg gctggatgat actactgagc aatcagagat tgagccagaa ccagaaccta   3240

cacctgaaga accagttaat cagtttactg gttatttaaa acttactgac aatgttgcca   3300

ttaaatgtgt tgacatcgtt aaggaggcac aaagtgctaa tcctatggtg attgtaaatg   3360

ctgctaacat acacctgaaa catggtggtg gtgtagcagg tgcactcaac aaggcaacca   3420

atggtgccat gcaaaaggag agtgatgatt acattaagct aaatggccct cttacagtag   3480

gagggtcttg tttgctttct ggacataatc ttgctaagaa gtgtctgcat gttgttggac   3540

ctaacctaaa tgcaggtgag gacatccagc ttcttaaggc agcatatgaa aatttcaatt   3600

cacaggacat cttacttgca ccattgttgt cagcaggcat atttggtgct aaaccacttc   3660

agtctttaca agtgtgcgtg cagacggttc gtacacaggt ttatattgca gtcaatgaca   3720

aagctcttta tgagcaggtt gtcatggatt atcttgataa cctgaagcct agagtggaag   3780

cacctaaaca agaggagcca ccaaacacag aagattccaa aactgaggag aaatctgtcg   3840

tacagaagcc tgtcgatgtg aagccaaaaa ttaaggcctg cattgatgag gttaccacaa   3900

cactggaaga aactaagttt cttaccaata agttactctt gtttgctgat atcaatggta   3960

agctttacca tgattctcag aacatgctta gaggtgaaga tatgtctttc cttgagaagg   4020

atgcacctta catggtaggt gatgttatca ctagtggtga tatcacttgt gttgtaatac   4080

cctccaaaaa ggctggtggc actactgaga tgctctcaag agctttgaag aaagtgccag   4140
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24

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25

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26

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27

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28

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29

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30

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31

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32

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<210>  21
<211>  30
<212>  DNA
<213>  SARS coronavirus

<400>  21
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<210>  22
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<400>  22
cgggatccga tccacaattc aaagacaac                                   29


<210>  23
<211>  31
<212>  DNA
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<400>  23
acgcgtcgac ttatgcctga gttgaatcag c                                31


<210>  24
<211>  32
<212>  DNA
<213>  SARS coronavirus


<220>
<221>  misc_feature
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<222>   (3)..(8)

<400>   24
cgggatccaa cgtcatactg ctgaacaagc ac                                         32


<210>   25
<211>   31
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<213>   SARS coronavirus


<220>
<221>   misc_feature
<222>   (5)..(10)

<400>   25
acgcgtcgac ttatgcctga gttgaatcag c                                          31
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